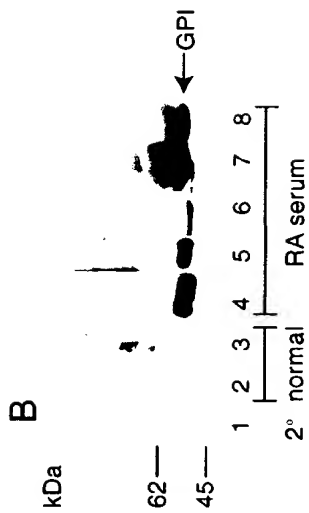


Fig. 1A



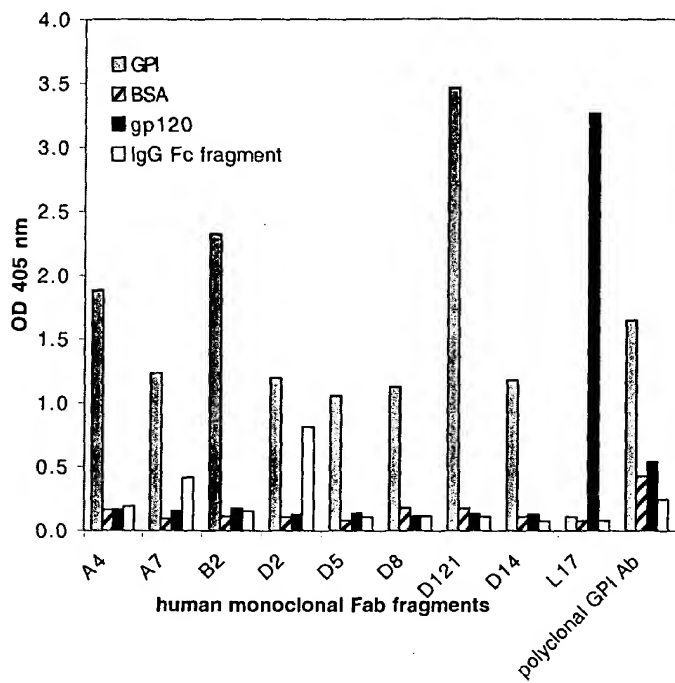


Fig. 2

FIG. 3AL
Light Chain Variable AA Sequences

<u>Name</u>	<u>SEQ ID NO.</u>	<u>FR1</u>	<u>CDR1</u>	<u>FR2</u>
A4	1	PDSLAVSLGERATINC	KSSQSVFYTSNNKNYLA	WYQQKPGQPPKLLIY
D2	2	PSFLSASVGDRVITTC	RASQGISSYLA	WYQLKPGKAPKLLIY
D121	3	PGTILSLPGERATLSC	RASQSVSSSYLA	WYQQKPGQAPRLLIY
B2	4	PDSLAVSLGERATINC	KSSQSVFYTSNNKNYLA	WYQQKPGQPPKLLIY
D14	5	PGTILSLPGEATLSC	RASQSVSSSYLA	WYQQRPGQAPRLLIY
D5	6	PGTILSLPGEATLSC	RASQSVSSSYLA	WYQQKPGQAPRLLIY
A7	7	PGTILSLPGERVTILSC	RASQSVSSSYLA	WYQQKPGQAPRLLIY

<u>Name</u> <u>cont'd</u>	<u>CDR2</u>	<u>FR3</u>	<u>CDR3</u>	<u>FR4</u>
A4	WASTRES	GVPDFRFGSGSGTDFTLTISSLQAEDVAVYYC	QYYYSYT	FGQGTKLEIKRTVA
D2	AATLQS	GVPSRFGSGSGTEFTLTISSLQPEDFATYYC	QQLNSYPLT	FGGGAKEVGIKRTVA
D121	GASSRAT	GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC	QYYGSSPRT	FGQGTKVEIKRTVA
B2	WASTRES	GVPDFRFGSGSGTDFTLTISSLQAEDVAVYYC	QYYYSYT	FGQGTKLEIKRTVA
D14	GASSRAT	GIPDRFSGSGSGTDFTISRLEPEDTGTYYC	QYYDNVPDT	FGQGTIRLEIKRTVA
D5	GASSRAT	GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC	QYYGTSPL	FGQGTIRLEIKRTVA
A7	GASSRAT	GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC	QYYGSSPRT	FGQGTKVEIKRTVA

FIG. 3AH
Heavy Chain Variable AA Sequences

Name	SEQ ID NO.	FR1	CDR1	FR2	CDR2
A4	8	GGGVVQPGRLKLSCAASGFTFS	SHGSH	WVRQAPGKGLEWVA	LLSSDGSNKFYIESVKG
D2	9AW..LR..V.....	..TM.TM.
D121	10R.....	.YTF.	VI.Y..NK.Y.AD.....
B2	11	GAEVKPKGTSVRLSCRASGNTFT	GHHIH	WVRQAPGQGLQWVG	RINPTGGGVSLAQSFQD
D14	12	GGGLVQPGGSLRLSCATSGFIFN	SYAMN	WVRQAPGKGLEWVS	RISGNSGSTFYADSVKG
D5	13	GPGLVRPSQTLTILTCVPSPGSIK	GDSYFWS	WVRQPVGKGLEWIG	RIYGRGTTNNRVFVS
A7	14	GAEVKPKGSSVKVSCRASGTFVS	RYAIS	WVRQAPGQGLEWVG	GIIPPGPVPVNYAQKFQG
Name	cont'd	FR3	CDR3	FR4	VH gene
A4	RFTISKDNSKNTLYLQMNRLRIDDYVYCAI		SLVGTTFAPNY	WGQGTLLTVSS	VH3
D2R.....LS..PE.....TN		.E..A....D.	VH3
D121VE.....		.I.....	VH3
B2	RVSLTRDRSSNTVFLESLGLEEDTALYFCAR		PRFNMIREPLDL	WGQGTVVTVSS	VH1
D14	RFTISRDNKNTAFIRMNSQRAEDTAVYICAK		DLSSGAYYYGMDV	WGQGTVVTVSS	VH3
D5	RVSMVDMRSRQFFLELRDVTAAATVYICAR		DKGSEYSYFDP	WGQGIIVNVFVS	VH4
A7	RVTITADDSTNTAYMGLSSLRSGDTAVYICAR		VAYDGSYYNNIPKIYYYSYMD	WGKGTVVTVSS	VH1

FIG. 3B

Name	SEQ ID NO.	FR1	CDR1	FR2	CDR2
A4	8	GGGVVQPGRSILKLSCAASGTFPS	SHGSH	WVRQAPGKGLEWVA	LLSSDGSNKFYIESVKG
D2	9AW..LR..V.....	..TM.		..TM.
D121	10R.....	.YTF.		VI.Y..NK.Y.AD....
DP-46	R.....	.YAM.		VI.Y.....AD....
B2	11	GAEVRKPGTSVRISCRASGNTFT	GHHIH	WVRQAPGQGLQWVG	RINPTGGGVSLAQSFQD
DP-7	K...A..KV..K...Y...	SYMHE...	I...S..ST.Y..K..G
D14	12	GGGLVQPGGSLRLSCATSGFIFN	SYAMN	WVRQAPGKGLEWVS	RISGNSGSTFYADSVKG
VH26	A...T.SS		A...SG...Y.....
D5	13	GPGLVRPSQTLTLCPVSPGSIK	GDSYFWS	WVRQFVGKGLEWIG	RIYGRGTTNYNRVFGS
IGHCAK	K.....T..G...S	SG..Y..	.I...A.....	...TS.S.....PSLK.
A7	14	GAEVKKPGSSVKVSCRASGGTFS	RYAIS	WVRQAPGQGLEWVG	GIIPPGFVNVYAQKFQG
VH1-69	K.....	S....I..TA.....

FIG. 3B CONT'D

Name cont'd	FR3	CDR3	FR4	VH gene
A4	RFTISKDNSKNTLYLQMNLSRIDDTAVYYCAI	SLVGTTFATNY	WGQGTFLVTVSS	VH3
D2R.....LS...PE.....TN	.E..A...D.	VH3
D121R.....VE.....	.I.....		VH3
DP-46R.....AE.....R			
B2	RVSLTRDRSSNTVFLELSGLTEEDTALYFCAR	PRFNMIREPLDL	WGQGTFLVTVSS	VH1
DP-7	..TM...T.TS..YM...S.RS...V.Y...			
D14	RFTISRDNKNTAFLRMNSQRAEDTAVYYCAK	DLSSGAYYYGGM	WGQGTFLVTVSS	VH3
VH26LY.Q...L.....	DV		
D5	RVSMVDMRSQFFLELRDVTAAQTAVYYCAR	DKGSEYSYFDP	WGQGIIVNVFS	VH4
IGHCAK	..TI...T.KN..S.K.SS.....			
A7	RVTITADDSTNTAYMGLSLRSGDTAVYYCAR	VAYDGSQYNNI	WGKGTFLVTVSS	VH1
VH1-69K..S....E.....E.....	PKIYYYSYMDV		

FIG. 3C

Clone	Closest Germline	% amino acid homology	% nucleotide homology	R/S ratio FRs	R/S ratio CDRs
A4	DP-46	86	89	6/6:1.0	12/5:2.4
D2	DP-46	87	92	8/6:1.3	4/5:0.8
D121	DP-46	91	95	2/4:0.5	7/0:>7.0
B2	DP-7	67	79	20/17:1.2	14/5:2.8
D14	VH26	87	93	7/3:2.3	5/2:2.5
D5	IGHCAK	73	81	17/16:1.1	13/4:3.3
A7	VH1-69	90	94	7/2:3.5	5/0:>5.0

FIG. 4A

CDR's Heavy Chain

SEQ ID	CDR1	SEQ ID NO:	CDR2	SEQ ID NO:	CDR3
15	SHGSH	22	LLSSDGSNKFYIESVKG	29	SLVGTTFN
16	.TM.	23	.IFY....Y.AD....	30	.E..A...D.
17	.YTF.	24	VI.Y..NK.Y.AD....	31	.I.....
18	GHHIH	25	RINPTGGVSLAQSFQD	32	PRFNMIREFLDL
19	SYAMN	26	RISGNSGSTFYADSVKG	33	DLSSGAYYYYGMDV
20	GDSYFWS	27	RIYGRGTTNVRVFGS	34	DKGSEYSYFDP
21	RYAIS	28	GIIPPFPGPVNYAQKFG	35	VAYDGSYNNIPKIYYYSYMDV

CDR's Light Chain

SEQ ID	CDR1	SEQ ID NO:	CDR2	SEQ ID NO:	CDR3
36	KSSQSVFYTSNNKNYLA	43	WASTRES	50	QQYDYSYT
37	RASQGISSYLA	44	AASTLQS	51	QQLNSYPLT
38	RASQSVSSSYLA	45	GASSRAT	52	QQYGSSPRT
39	KSSQSVFYTSNNKNYLA	46	WASTRES	53	QQYDYSYT
40	RASQSVSSSYLA	47	GASSRAT	54	QQYDNVPDT
41	RASQSVSSSYLA	48	GASSRAT	55	QQYGTSPIL
42	RASQSVSSSYLA	49	GASSRAT	56	QQYGSSPRT

FIG. 4B
Framework Regions, Heavy Chain

SEQ ID	FR1	SEQ ID	FR2
NO:		NO:	
57	GGGVQPGRSLKLSCAASGFTFS	64	WVRQAPGKGLEWVA
58AW..LR...V.....	64
59R.....	64
60	GAEVKPGTSVRISCRASGNTFT	65	WVRQAPGQGLQWMG
61	GGGLVQPQGSRLSCATSGFIFN	66	WVRQAPGKGLEWVS
62	GPGLVRPSQTLSLTCVPSPGSIK	67	WVRQPVGKGLEWIG
63	GAEVKKPGSSVKVSCRASGTFFS	68	WVRQAPGQGLEWMG
SEQ ID	FR3	SEQ ID	FR4
NO:		NO:	
69	RFTISKDNKNTLYLQMNSLRIDDTAVYYCAI	76	WGQGTLLVTVSS
70R.....LS..PE.....TN	76
71VE.....	76
72	RVSLTRDRSSNTVFLELSGLTEEDTALYFCAR	77	WGQGTVVTVSS
73	RTIISRDNSKNTAFLRMNSQRAEDTAVYYCAK	78	WGQGTTVTVSS
74	RVMSVDMRSQFFLELRDVTADTAVYYCAR	79	WGQGIVVNVFS
75	RVITITADDSTNTAYMGLSSLRSGDTAVYYCAR	80	WGKGTTVTVSS

FIG. 4B cont'd
Framework Regions, Light Chain

SEQ ID NO:	FR1	SEQ ID NO:	FR2
81	PDSLAVSLGERATINC	88	WYQKPGQPPKLLIY
82	PSFLSASVGDRTITC	89	WYQLKPGKAPKLLIY
83	PGTSLSPGERATLSC	90	WYQKPGQAPRLLIY
84	PDSLAVSLGERATINC	91	WYQKPGQPPKLLIY
85	PGTSLSPGEGATLSC	92	WYQRPQGAPRLLIY
86	PGTSLSPGEGATLSC	93	WYQKPGQAPRLLIY
87	PGTSLSPGERVTLSC	94	WYQKPGQAPRLLIY
SEQ ID NO:	FR3	SEQ ID NO:	FR4
95	GVPDRFSGSGGTDFTLTISSLQAEDVAVYYC	102	FGQGTKLEIKRTVA
96	GVPSRFSGSGGTEFTLTISSLQPEDFATYYC	103	FGGGAKEVGIRRTVA
97	GIPDRFSGSGGTDFTLTISRLEPEDFAVYYC	104	FGQGTKVEIKRTVA
98	GVPDRFSGSGGTDFTLTISSLQAEDVAVYYC	105	FGQGTKLEIKRTVA
99	GIPDRFSGSGGTDFTISLQPEDTGTYTC	106	FGQGTRELKRTVA
100	GIPDRFSGSGGTDFTLTISRLEPEDFAVYYC	107	FGQGTRELKRTVA
101	GIPDRFSGSGGTDFTLTISRLEPEDFAVYYC	108	FGQGTKVEIKRTVA

FIG. 5A

LIGHT CHAIN NUCLEOTIDE SEQUENCE OF ANTI-GPI ANTIBODIES

A4 - SEQ ID NO:112

CCAGACTCCCTGGCTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTGTGTTTTTACACTTCCAAACAATAA
GAACTACTTATAGTTGGTACCAAGCAAGAAACAGGCCAGCCTCTAAAGTTGCTCATTTTACTGGGCATCCACCCGGGAATCCGGGGTCC
CTGACCGATTGAGTGGCAGCGGTCTGGGACAGATTTCATCTCAACATCAGCAGCCTGCAAGTGAAGATGTGGCAGTTTATTAC
TGTACGCAATATTATGATTCTGACACTTTTGGCCAGGGGACCAAGCTGGAGATCAAAACGAACCTGTGGCT

D2 - SEQ ID NO:113

CCATCCTTCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGGCCAGTCAAGGCATTAGCAGTTATTTAGCCTGGTAT
CAGCTAAAACCGGGAAAGCCCTTAAGCTCCTGATCTATGCTGCATCCACTTTGCAAGTGGGTCCCATCAAGGTTTCAGCGGCAG
TGGATCTGGGACAGAAATTCATCTCACAATAAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACTGTCAACAGCTTAATAGTT
ACCTCTCACTTTCCGGGAGGGGCCAAGGTGGGGATCAGACGAACTGTGGCT

D121 - SEQ ID NO:114

CCAGGCACCCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGCTACTTAGCCTG
GTACCAAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATCTATGTTGCATCCAGCAGGGCCACTGGCATCCCAAGCAGGTTTCAGTG
GCAGTGGTCTGGGACAGACTTCATCTCACCATCAGCAGCTGGAGCCTGAAGATTTTGCAAGTGTATTACTGTGACGAGTATGGT
AG CTCACCTCGGACGTTCTGGCCAAAGGACCAAGGTGGAAATCAAAACGAACTGTGGCT

B2 - SEQ ID NO:115

CCAGACTCCCTGGCTGTCTCTGGGCGAGAGGGGCCACCATCAACTGCAAGTCCAGCCAGAGTGTGTTTTTACACTTCCAAACAATAA
GAACTACTTATAGTTGGTACCAAGCAAGAAACAGGCCAGCCTCTAAAGTTGCTCATTTACTGGGCATCCACCCGGGAATCCGGGGTCC
CTGACCGATTGAGTGGCAGCGGTCTGGGACAGATTTCATCTCAACATCAGCAGCCTGCAAGCTGAAGATGTGGCAGTTTATTAC
TGTACGCAATATTATGATTCTGACACTTTTGGCCAGGGGACCAAGCTGGAGATCAA ACGAACTGTGGCT

FIG. 5A cont'd

D14 - SEQ ID NO:116

CCAGGCACCCTGTCATTGTCTCCAGGGGAAGGAGCCACCCTCTCCTGCAAGGGCCAGTCAGAGTGTTAGCAGCAGCTACCTAGCCTG
GTATCAGCAGAGACCTGGCCAGGCTCCAGGCTCCTCATCTATGGTGCCATCCAGAGGGCCACCGGCATCCAGACAGATTTCAGTG
GAAGTGGATCTGGGACAGATTTCAGTTTCACCATCAGCAGTCTGAGCCTGAAGATACTGGACATATTACTGTCAACAATATGAT
AATGTCCCTGACACTTTTGGCCAGGGACCAGGCTGGAGATCAACGAACTGTGGCT

D5 - SEQ ID NO:117

CCAGGCACCCTGTCATTGTCTCCAGGGGAAGGAGCCACCCTCTCCTGCAAGGGCCAGTCAGAGTGTTAGCAGCAGCTACTTAGCCTG
GTACAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATCTATGGTGCCATCCAGTAGGGCCACTGGCATCCAGACAGGTTTCAGTG
GCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAAGCAGTATGGT
ACCTCACCCCTCTCGGCCAAGGGACACGACTGGAGATTAAACGAACTGTGGCT

A7 - SEQ ID NO:118

CCAGGCACCCTGTCATTGTCTCCAGGGGAAGAGTCACTCTCCTGCAAGGGCCAGTCAGAGTGTAGCAGCAGTACTTAGCCTG
GTACAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATCTATGGTGCCATCCAGCAGGGCCACTGGCATCCAGACAGGTTTCAGTG
GCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGACTTTGCAGTGTATTACTGTCAAGCAGTATGGA
AGCTCACCTCGGACGTTGGCCAGGGACCAAGGTGGAAATCAACGAACTGTGGCT

FIG. 5B

HEAVY CHAIN NUCLEOTIDE SEQUENCE OF ANTI-GPI ANTIBODIES

A4-H – SEQ ID NO:116

GAGGCGTGGTCCAGCCTGGGAGGTCCCTGAAACTCTCCTGTGCAGCCTCTGGATTACATTCAAGTAGTCATGGCTGGCACTGGGTC
CGCAAAGCTCCAGGCAAGGGGCTGGAGTGGGTGGCACTTTTGTCTGTGATGGAAAGTAATAATTCTATATAGAAATCCGTGAAGG
GCCGATTACCATCTCCAAGGACAATTCTAAGAACACACTGTATCTGCAAAATGAACAGCCTGAGAATTGACGACACGGCTGTCTAT
TACTGTGGGATTTCCCTGGTGGGAACTACCGCTTTTAACACTACTGGGGCCAGGGAAACCCTGGTCAACCGTCTCTCA

D2-H – SEQ ID NO:117

GGCGTGGTCCAAAGCATGGAGGTCCCTAAGACTCTCCTGTGTAGCCTCTGGATTACCTTCAGTAGTCATACCATGCATGGGTCCG
CCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCACTTATATCTATGATGGAAAGTAATAATACTATGACAGCTCCGTGAAGGC
CGATTCAACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAATTGAGCAGCCTAAGACCTGAGGACACGGCTGTCTATTA
TTGTACGAATTCGAGGTGGGAGCTACCGCTTTTGTACTACTGGGGCCAGGGAAACCCTGGTCAACCGTCTCTCAG

D121-H – SEQ ID NO:118

GGGAGGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTTTTCTGTGCGCCCTCTGGATTCACTTCAGTTCCTATATCTTCCACTGG
GTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCACTTATATCATATGATGGAAACAAAGAAATACTACGCAGACTCCGTGA
AGGGCCGATTCAACATCTCCAGAGACAATTCCAAGAACACTCTATATCTGCAAAATGAACAGCCTGAGAGTTGAGGACACGGCTGT
TATTACTGTGCGATTTCCATAGTGGAACTACCGCTTTTAACTACTGGGGCCAGGGAAACCCTGGTCAACCGTCTCTCCTC

B2-H – SEQ ID NO:119

GGGGTGAGGGTGAGGAAGCCCGGACCTCCGTGAGGATCTCTTGCAAGGCATCTGGAAACACCTTCACTGGCCACCATATTCAC
GGTCCGCCAGGCCCTGGACAAGGCTTCAGTGGATGGGAAGAAATCAACCCGACTGGCGGCGGCTTAGTCTCGCACAGAGTTTC
CAGGACAGAGTCAGCCTGACACAGGACAGGTGCTCCAATACAGTCTTCTTGGAACCTGAGCGGCCCTCACGGAGGAGGACACGGCCT
TATATTCTGTGCGAGGCCCGATTTAACATGATCCGGAAACCTCTTGACCTCTGGGGCCAGGGGACAGTGGTCAACCGTCTCCTCA

D14-H – SEQ ID NO:120

GGGGAGGCTTGGTACAGCCTGGGGGTCCCTGAGACTCTCCTGTGCAACCTCTGGATTTCATCTTTAACAGCTATGCCATGAACCTG
GGTCCGCCAGGCTCCAGGGAAGGGCTTGAGTGGTCTCACGTAATTAGTGAATAAGTGAAGCACATTCACGCAGACTCCGTG
AAGGCCGGTTCAACATCTCCAGAGACAAATCCAAGAACACGGCGTTTCTGCGAATGAACAGCCAGAGAGGCCGAAGACACGGCCG
TTTATTACTGTGCGAAAGATCTGTGAGTGGTGCCATACTACTACGGGATGGACGTCTGGGGCCAAAGGACCAACGGTCAACCGTC
TCCTCA

D5-H – SEQ ID NO:121

GGCCCAGGATTGGTGAGGCCATCACAGACCTATCCCTCACCTGCACCTGTCTCTCCAGGCTCCATTAAAGGTGATAGTTACTTCTGG
AGCTGGGTCCTGACGCCGTAGGGAAGGGACTGGAGTGGATAGGGCGTATCTACGGCAGAGGGACTACCAATTACAACCGTGTTT
TCGGGAGTCGAGTCAGTATGTCA GTGGACATGTCCAGGAGTCAGTTTTCTTGAAATTGAGAGATGTGACCGCCGACAGACACGGCC
GTCTATTACTGTGCGAGAGACAAGGGGTCCGAATACTCCTACTTTGACCCCTGGGGCCAGGGAATAGTGGTCAACCGTCTTCTCA

A7-H - SEQ ID NO:122

FIG. 5B CONT'D

GGGCTGAGGTGAAGAAGCCTGGTCTCGAGGCTCTTGGAGGCACATTCAGCAGATATGCTA
TCAGCTGGGTGGACAGGCCCTGGACAAAGGCTTGTAGTGTAGGAGGATCATCCCTCCTTGTGCAGTAAACT
ACGCACAGAAGTTCCAGGGCAGTACAGATTACCGCGACGATTCCACGAACACAGCTACTACGGTCTGAGCAGCC
TGAGCTCGGGACACGCCCGTGTATTACTGCGCAGAGTGGCTATGATGTTATCAACAATATCCCAA
AGATCTACTACTCTCATGTGACGTCTGGGGCAAAAGGACACCGTCAACCGTGTCTCAGC

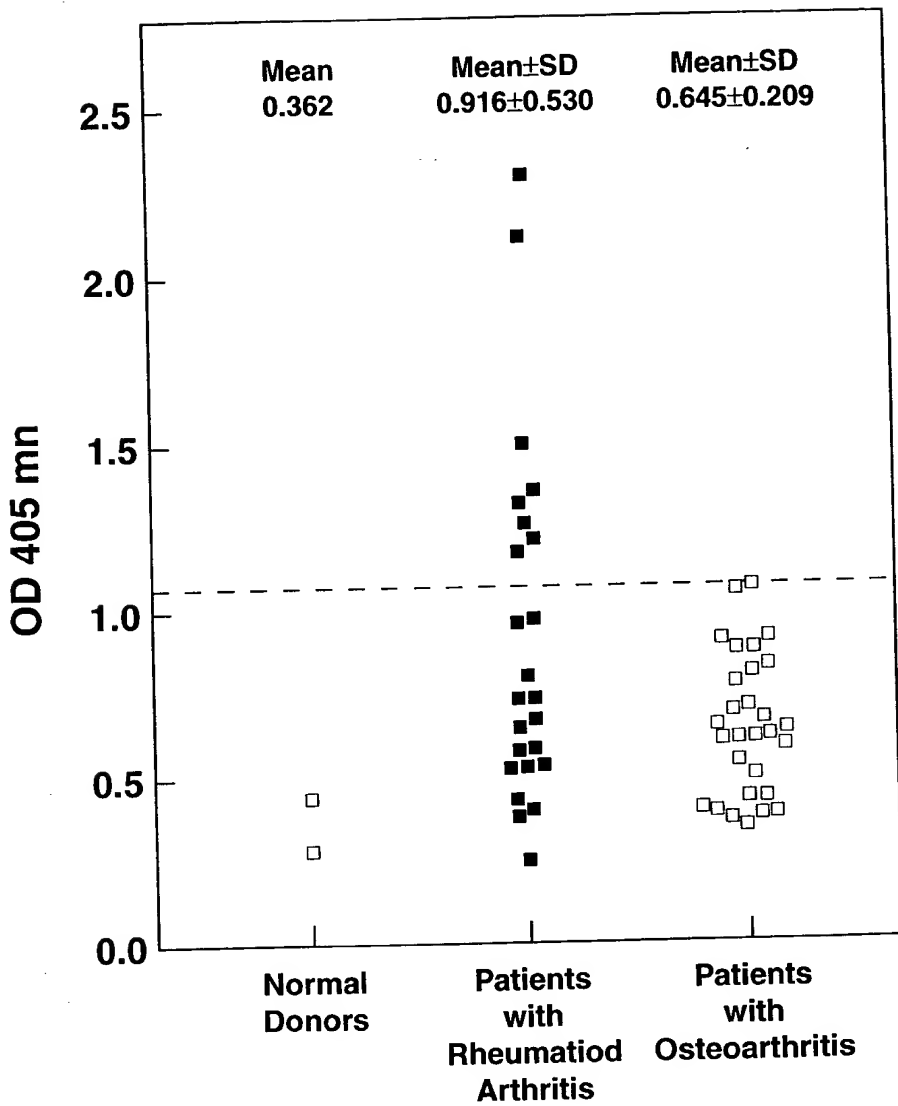


Fig. 6

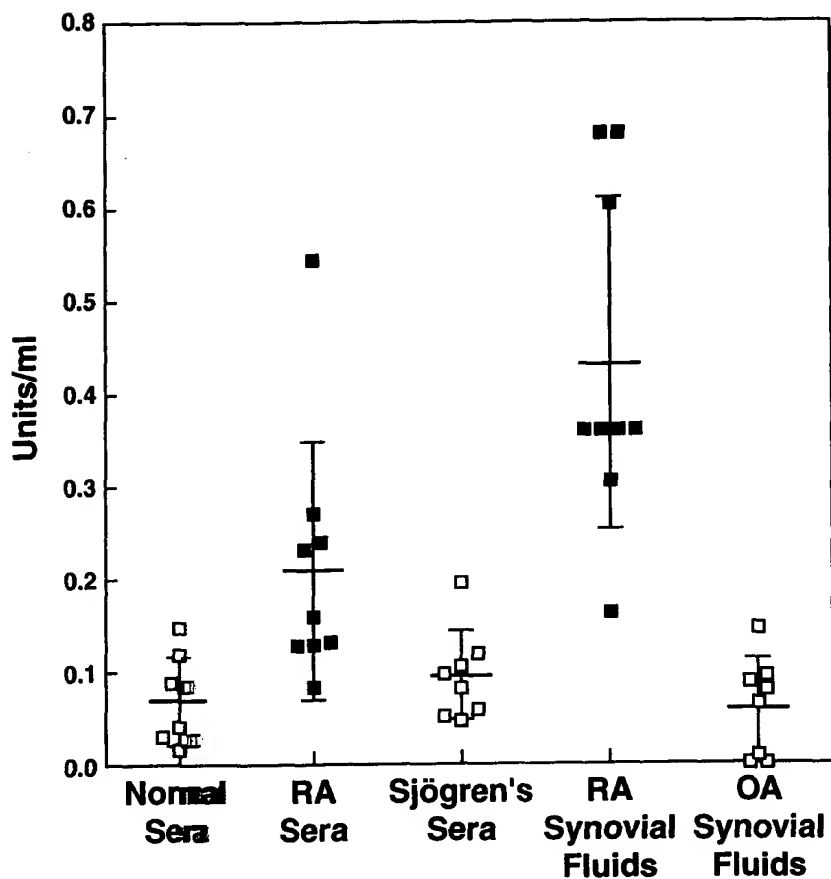


Fig. 7

103040-20432250

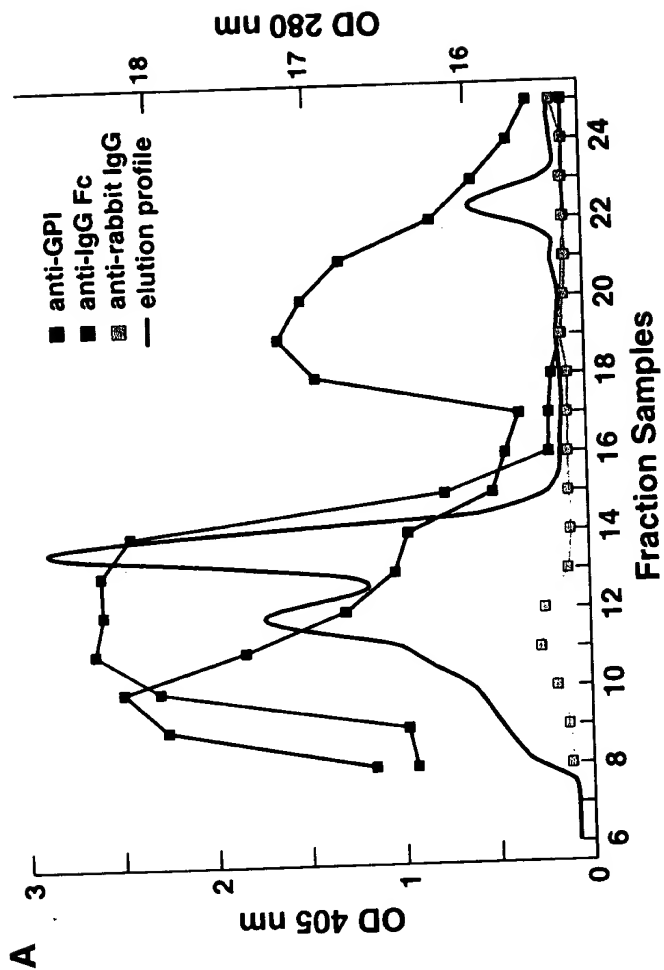


Fig. 8

110010"00430050

Fig 9

